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 Db 1861 TTGGCCATTGTATGATGTTAACATGGATAATGAATTGTGACTT 1920
 Qy 1905 CTGTCAGAAGAACAGAGGTAACATTCTCATTAAATTTAACATGGATAATGAATTGTGACTT 1964
 Db 1921 CTGTCAGAAGAACAGAGGTAACATTCTCATTAAATTTAACATGGATAATGAATTGTGACTT 1980
 Qy 1965 AAAAAAAAAAAAAAAA 1994
 Db 1981 TTGTGACTTGTAAACAGATGACAGAA 2010

RESULT 4
 HUM3H3M LOCUS Homo sapiens 3-hydroxy-3-methylglutaryl coenzyme A synthase mRNA, DEFINITION complete cds.
 ACCESSION 125798
 VERSION 125798.1 GI:410027
 KEYWORDS 3-hydroxy-3-methylglutaryl coenzyme A synthase.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1650)
 AUTHORS Rokosz,L.I., Boulton,D.A., Butkiewicz,E.A., Sanyal,G., Cueto,M.A.,
 Lachance P. A. and Hermes J. D.
 TITLE Human cytoplasmic 3-hydroxy-3-methylglutaryl coenzyme A synthase: expression, Purification, and characterization of recombinant wild-type and Cys129 mutant enzymes
 JOURNAL Arch. Biochem. Biophys. 312 (1), 1-13 (1994)
 MEDLINE 94304177
 PUBMED 7913309
 COMMENT Original source text: Homo sapiens fetal adrenal cDNA to mRNA.
 FEATURES Location/Qualifiers
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 RMLINDFINDQRDKNSIYSLEAFDVKLDTYEDDEKEFKMSSLFSQKTRAS
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ORIGIN

Query Match 68.4%; Score 1370; DB 9; Length 1650;
 Best Local Similarity 92.0%; Pred. No. 1e-287; 5; Indels 16; Gaps 1;
 Matches 1509; Conservative 0; Mismatches 0; CTCATTTGATGAAAGATG 193
 Db 11 GCTCTTTTCAACCAGCTGGATCACTTCCCTGGATCACTTGGCCAAAGATG 70
 Qy 194 TGGGAAATTGTGGCTTGTGATGAAAGATGCTTCAATATGTTGATCAAGGAGATG 253
 Db 71 TGGGATTTGTGGCTTGTGATCTTCAATATGTTGATCAAGGAGATG 130
 Qy 254 AAAAATATGATGATGCTGAGTAGTACCATGGCTGGCAAGCCAGATGG 313
 Db 131 AAAATATGATGATGCTGAGTAGTACCATGGCTGGCAAGCCAGATGG 190

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 Db 191 GCTTGTGACAGATGAGAGATTAATCTCTTGGATGACTCTCTTGCATCTCTTA 250
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 12:56:26 ; Search time 44 Seconds

(Without alignments)
565.671 Million cell updates/sec

Title: US-10-622-516-2

Perfect score: 2511

Sequences: 1 MFGSLPLNAAECWPKDVGIV. PRLPATAEPEAVISNGEH 478

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

141681 seqs, 5207055 residues

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SwissProt_42.2*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2480	98.8	520	1	HMCS_HUMAN	Q01581 homo sapien
2	2362	94.1	520	1	HMCS_RAT	P17415 rattus norvegicus
3	2352	93.7	520	1	HMCS_CHICK	P13704 cricetus
4	2097	83.5	522	1	HMCS_HUMAN	P23228 gallus gallus
5	1513	60.3	508	1	HMCM_RAT	P54868 homo sapien
6	1494	59.5	508	1	HMCM_RAT	P22771 rattus norvegicus
7	1493	59.5	480	1	HMCM_MOUSE	P054869 mus musculus
8	1466	58.4	508	1	HMCM_PIG	P02734 sus scrofa
9	1352.5	53.9	453	1	HMCL_BLAZE	P54961 biatella g
10	1272.5	50.7	455	1	HMCL_BLAZE	P54870 blattella g
11	980	39.0	461	1	HMCS_YARTH	P54873 arabidopsis thaliana
12	950.5	37.9	491	1	HMCS_YARTH	P54833 sacharomyces cerevisiae
13	900	35.8	447	1	HMCS_SCHEPO	P54874 schizosaccharomyces pombe
14	705	28.1	462	1	HMCS_DICDI	P54971 caenorhabditis elegans
15	249	9.9	163	1	YD79_METKA	P54872 dictyostelia metzgeri
16	152	6.1	350	1	Q8tv10_methanopyruvate	P08tv10 methanopyruvate reductase
17	147	5.9	345	1	PRSG_BACSU	P240820 bacillus subtilis
18	145.5	5.8	346	1	Y792_METTH	Q26882 methanobacter thermoautotrophicum
19	144	5.7	350	1	Y677_PTYRHO	Q58410 pyrococcus abyssi
20	138.5	5.5	350	1	Y912_PYRFU	P051738 pyrococcus furiosus
21	135	5.4	349	1	YB71_METMA	Q8pyj0 methanospirillum thermophilum
22	132.5	5.3	343	1	Y015_ARCFU	P30256 archaeoglobus fulgidus
23	130	5.2	350	1	YLBS_PYRAE	Q8zrp4 pyrobaculum aerophilum
24	127	5.1	349	1	Y4E1_METAIC	Q8tivo methanospirillum thermophilum
25	126.5	5.0	350	1	YD69_PYRAB	Q9uyys pyrococcus abyssi
26	123.5	4.9	350	1	BGAL_THETTU	P26257 thermoaerobacter ethanolicus
27	123	4.9	351	1	Y132_THEVO	Q97cg9 thermoplasmatales
28	122	4.9	351	1	YF46_METUA	Q58941 methanococcus capsulatus
29	122	4.9	351	1	YE55_THEAC	Q9hi87 thermoplasmatales
30	121	4.8	580	1	NO56_MOUSE	Q9dzl1 mus musculus
31	118.5	4.7	595	1	NO56_HUMAN	Q00567 homo sapiens
32	116	4.6	348	1	YD49_SULTO	Q97k88 sulfolobus solfataricus
33	107.5	4.3	454	1	TOP1_RICPR	Q9zd2c rickettsia

ALIGNMENTS

34	106.5	4.2	1517	1	GLTB_ECOLI	P09831 escherichia coli
35	106	4.2	367	1	YQL2_CAEEL	Q09291 caenorhabditis elegans
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37	105	4.2	3358	1	PGCY_MOUSE	Q6259 mouse
38	103	4.1	489	1	YSV5_CAEEL	Q10011 caenorhabditis elegans
39	103	4.1	1197	1	DPDN_PODAN	Q01529 podospira aerophila
40	102	4.1	360	1	HIS8_LACLA	Q9x355 lactococcus lactis
41	102	4.1	1163	1	C0BA_BACTP	Q9x597 bacillus thuringiensis
42	101	4.0	365	1	YI73_AERPE	Q9yaso aeropyrum
43	100.5	4.0	776	1	TOP1_RICCN	Q92ih1 rickettsia conopi
44	100	4.0	1136	1	CABA_BACTI	P05519 bacillus thuringiensis
45	99.5	4.0	494	1	ILVC_VIBPA	Q87tn4 vibrio parahaemolyticus

RESULT 1
ID HMCS_HUMAN STANDARD PRT: 520 AA.

AC 001581; Rel: 26, Created)

DT 01-JUL-1993 (Rel: 34, Last sequence update)

DT 01-OCT-1996 (Rel: 42, Last annotation update)

DE Hydroxymethylglutamyl CoA Synthase, Cyttoplasmic (EC 2.3.3.10) (HMG-CoA synthase)

DE (3-hydroxy-3-methylglutaryl coenzyme A synthase).

GN HMCCS1 OR HMGCSC.

OC Homo sapiens (Human).

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OC NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Fetal adrenal gland, Human.

RC MEDLINE=93041939; PubMed=91358203;

RA Russ A.P., Ruzicka V., Maerz W., Appelhans H., Gross W.,

RA "Amplification and direct sequencing of a cDNA encoding human cytosolic 3-hydroxy-3-methylglutaryl-coenzyme A synthase." Biophys Acta 1132:329-331(1992).

RN [2] SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.

RC TISSUE=Fetal adrenal gland, Human.

RC MEDLINE=9430197; PubMed=913309;

RA Rokosz L.L., Boulton D.A., Butkiewicz E.A., Sanyal G., Cueto M.A.,

RA "Lachance P.A., Hermesz E.J.D., Moore T., Max S.I., Wang J., Hsieh F.,

RA "Human cytoplasmic 3-hydroxy-3-methylglutaryl coenzyme A synthase: expression, purification, and characterization of recombinant wild-type and Cy129 mutant enzymes." Arch. Biochem. Biophys. 312:1-13(1994).

RL Sequence FROM N.A.

RC TISSUE=lung;

RC STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Bhat N.K., Hopkins R.F., Zeberg B.B., Buetow K.W., Schaefer C.M., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soresi M.B., Bonaldo M.F., Casavant T.L., Brownstein M.J., Usdin T.B., Toshimori S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhahy S.J., Bosak S.A., McBryan P.J., McKernan K.J., Malek J.A., Garcia A.M., Hale S., Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Fahy J., Heitman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL

-!- FUNCTION: This enzyme condenses acetyl-CoA with acetoacetyl-CoA to form HMG-CoA, which is the substrate for HMG-CoA reductase.
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + acetoacetyl-CoA = (S)-3-hydroxy-3-methylglutaryl-CoA + CoA
 CC -!- PATHWAY: PRODUCTION OF MEVALONATE FROM HMG-COA PRIOR TO THE SYNTHESIS OF STEROLS SUCH AS CHOLESTEROL AND ISOPRENOIDS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the HMG-CoA synthase family.

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 CC DR: X64435; CAA40611; -
 EMBL; BC00297; L25798; AAA64411; -
 DR: GO:0005737; C:cytoplasm; TAS.
 DR: GO:0005625; C:soluble fraction; TAS.
 DR: GO:0004421; F:hydroxymethylglutaryl-CoA synthase activity; TAS.
 DR: InterPro; IPR000590; HMG CoA synt AS.
 DR: InterPro; IPR008660; HMG CoA synt.
 DR: Pfam; PF01154; HMG CoA synt.; 1.
 PROSITE: PS01226; HMG CoA SYNTHASE; 1;
 KW Transferase; Cholesterol Biosynthesis; Multigene family.
 FT ACT SITE; 129 129 C->A; S: LOSS OF ACTIVITY.
 FT MUTAGEN; 129 129 G-> A (IN REF. 1).
 FT CONFLICT; 248 248 K-> N (IN REF. 1).
 FT CONFLICT; 251 251 E -> K (IN REF. 1).
 FT CONFLICT; 299 299 O -> H (IN REF. 1).
 FT CONFLICT; 364 364 P -> Q (IN REF. 1).
 FT CONFLICT; 420 420 EH -> VV (IN REF. 1).
 FT CONFLICT; 519 520 AA; 57293 MW; C6569212EP86CFF9B CRC64;
 SQ SEQUENCE; -----;

Query Match Score 2480; DB 1; Length 520;

Best Local Similarity 91.9%; Pred. No. 2.3e-173; Gaps 1; Mismatches 478; Conservative 0; Indels 42; Gaps 1;

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Qy 1 MGSLPLNAAACWPKDVGIVALEIYFPQSYDQAELEYKDGDAKGTYTGIGQAKMGPCT 60

Qy 61 DREDINSLCMTVQNIMERNLSPYCIGRLLEVGETIDKSKSVTKTNLQMFESGNTDI 120

Db 61 DREDINSLCMTVQNIMERNLSPYCIGRLLEVGETIDKSKSVTKTNLQMFESGNTDI 120

Qy 121 EGIDTNACGGTAAYFNAWNWIESSWDGRYALVAGDTAVATGNRPTGSGAVALL 180

Db 121 EGIDTNACGGTAAYFNAWNWIESSWDGRYALVAGDTAVATGNRPTGSGAVALL 180

Qy 150 -----GLRGPHMQLAYDFYKPDMLSEPYTDGKLSIQCYLSALDRCSVYCKI 198

Db 181 IGPNALIFERGLRGLTHMQAYDFYKPDMLSEPYTDGKLSIQCYLSALDRCSVYCKI 240

Qy 199 HAQWQEGNDQDFTINDFGFMIFHEPYCKVQSKLARMILINDQNDRKNSTYGLEA 258

Db 241 HAQWQEGNDQDFTINDFGFMIFHEPYCKVQSKLARMILINDQNDRKNSTYGLEA 300

Qy 259 FGDVKLEDTYFDVKEKAFAKRSSELFQSKTKASLLVSNONGNMNTSSYGSLSVLAQY 318

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Db 361 SPQLACKRISPVSYGSGLATLYSLKVTOQDATPGSALDKITASCDLKSRDLSDRTGVAP 420

RESULT 2	
HMCS RAT	STANDARD;
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AC P17435;	520 AA.
DT 01-AUG-1990 (Rel. 15, Created)	
DT 01-AUG-1990 (Rel. 15, Last sequence update)	
DT 10-OCT-2003 (Rel. 42, Last annotation update)	
DE Hydroxymethylglutaryl-CoA synthase, cytosolic (EC 2.3.3.10) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase).	
DE synthase	
DE Rattus norvegicus (Rat).	
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthidae; Rodentia; Sciurognathi; Muridae; Rattus.	
OC NCBInfo TaxID=10116;	
OX	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Sprague-Dawley; TISSUE=Liver;	
RC MEDLINE=90301491; PubMed=11972979;	
RA Ayte J., Gil J., Gomez G., Hegardt P.G.,	
RA "Nucleotide sequence of a rat liver cDNA encoding the cytosolic 3-	
RA hydroxy-3-methylglutaryl coenzyme A synthase."	
RA Nucleic Acids Res. 18:3642-3642 (1990).	
CC -!- FUNCTION: This enzyme condenses acetyl-CoA with acetoacetyl-CoA to form HMG-CoA, which is the substrate for HMG-CoA reductase.	
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + acetoacetyl-CoA = (S)-3-	
CC hydroxy-3-methylglutaryl-CoA + CoA.	
CC -!- PATHWAY: PRODUCTION OF MEVALONATE FROM HMG-COA PRIOR TO THE SYNTHESIS OF STEROLS SUCH AS CHOLESTEROL AND ISOPRENOIDS.	
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.	
CC -!- SIMILARITY: Belongs to the HMG-CoA synthase family.	
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC or send an email to license@isb-sib.ch).	
CC EMBL; X52625; CA3652.1; -	
DR PIR: S12736; S12736.	
DR InterPro; IPR000590; HMG_CoA_synt_AS.	
DR InterPro; IPR008260; HMG_CoA_synt.	
DR Pfam; PF01154; HMG_CoA_synt_1.	
DR PROSITE; PS01226; HMG_CoA_SYNTHASE_1.	
DR Transfase; Cholesterol Biosynthesis; Multigene family.	
FT ACT SITE 129 129 POTENTIAL ACT SITE 129 129 MW; CB213A2/B0C17CB CRC64;	
SQ SEQUENCE 520 AA; 57293 MW; C6569212EP86CFF9B CRC64;	
Query Match Score 94.1%; Best Local Similarity 87.5%; Gaps 1; Gaps 1;	
Matches 455; Conservative 11; Mismatches 12; Indels 42; Gaps 1;	
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Db 1 MGSLPLNAAACWPKDVGIVALEIYFPQSYDQAELEYKDGDAKGTYTGIGQAKMGPCT 60	
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Db 61 DREDINSLCMTVQNIMERNLSPYCIGRLLEVGETIDKSKSVTKTNLQMFESGNTDI 120	
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Db 121 EGIDTNACGGTAAYFNAWNWIESSWDGRYALVAGDTAVATGNRPTGSGAVALL 180	
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Db 181 IGPNALIFERGLRGLTHMQAYDFYKPDMLSEPYTDGKLSIQCYLSALDRCSVYCKI 240	
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Db 241 HAQWQEGNDQDFTINDFGFMIFHEPYCKVQSKLARMILINDQNDRKNSTYGLEA 300	
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Db 301 FGDKLEDTYFDVKEKAFAKRSSELFQSKTKASLLVSNONGNMNTSSYGSLSVLAQY 360	
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Db 361 SPQLACKRISPVSYGSGLATLYSLKVTOQDATPGSALDKITASCDLKSRDLSDRTGVAP 420	

Fig 3